



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/936,759	11/07/2001	Richard A. Jefferson	076518-0150	8995
39124 : 7590 02/16/2005 CAROL NOTTENBURG 814 32ND AVE 5 SEATTLE, WA 98144			EXAMINER VOGEL, NANCY S	
			ART UNIT 1636	PAPER NUMBER
DATE MAILED: 02/16/2005				

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/936,759	JEFFERSON ET AL.	
	Examiner	Art Unit	
	Nancy T. Vogel	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 36,37 and 60-63 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 36,37 and 60-63 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on ____ is/are: a) ☐ accepted or b) ☒ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. ____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. ____. |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| Paper No(s)/Mail Date <u>9/12/02, 4/26/02</u> . | 6) <input checked="" type="checkbox"/> Other: <u>seq. alignment</u> . |

DETAILED ACTION

Claims 36, 37, and 60-63 are pending in the case.

Information Disclosure Statement

Receipt of Information disclosure statements on 9/12/02 and 4/26/02 is acknowledged. Certain citations have not been considered, since copies have not been received. These citations have been struck through and the information referred to therein has not been considered.

Drawings

New corrected drawings in compliance with 37 CFR 1.121(d) are required in this application because the text of some of the drawings cannot be read (Figures 5 and 5c). Applicant is advised to employ the services of a competent patent draftsman outside the Office, as the U.S. Patent and Trademark Office no longer prepares new drawings. The corrected drawings are required in reply to the Office action to avoid abandonment of the application. The requirement for corrected drawings will not be held in abeyance.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:

Art Unit: 1636

It improperly lists a US patent application, 09/270,957, as a foreign application to which applicants claim benefit under 35 USC 119 (a-d).

Priority

It is noted that this application appears to claim subject matter disclosed in prior Application No. 09/270,957, filed 3/17/99. A reference to the prior application must be inserted as the first sentence of the specification of this application or in an application data sheet (37 CFR 1.76), if applicant intends to rely on the filing date of the prior application under 35 U.S.C. 119(e) or 120. See 37 CFR 1.78(a). For benefit claims under 35 U.S.C. 120, the reference must include the relationship (i.e., continuation, divisional, or continuation-in-part) of all nonprovisional applications. Also, the current status of all nonprovisional parent applications referenced should be included.

If the application is a utility or plant application filed under 35 U.S.C. 111(a) on or after November 29, 2000, the specific reference to the prior application must be submitted during the pendency of the application and within the later of four months from the actual filing date of the application or sixteen months from the filing date of the prior application. If the application is a utility or plant application which entered the national stage from an international application filed on or after November 29, 2000, after compliance with 35 U.S.C. 371, the specific reference must be submitted during the pendency of the application and within the later of four months from the date on which the national stage commenced under 35 U.S.C. 371(b) or (f) or sixteen months from the filing date of the prior application. See 37 CFR 1.78(a)(2)(ii) and (a)(5)(ii). This

time period is not extendable and a failure to submit the reference required by 35 U.S.C. 119(e) and/or 120, where applicable, within this time period is considered a waiver of any benefit of such prior application(s) under 35 U.S.C. 119(e), 120, 121 and 365(c). A priority claim filed after the required time period may be accepted if it is accompanied by a grantable petition to accept an unintentionally delayed claim for priority under 35 U.S.C. 119(e), 120, 121 and 365(c). The petition must be accompanied by (1) the reference required by 35 U.S.C. 120 or 119(e) and 37 CFR 1.78(a)(2) or (a)(5) to the prior application (unless previously submitted), (2) a surcharge under 37 CFR 1.17(t), and (3) a statement that the entire delay between the date the claim was due under 37 CFR 1.78(a)(2) or (a)(5) and the date the claim was filed was unintentional. The Director may require additional information where there is a question whether the delay was unintentional. The petition should be addressed to: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450.

Specification

The amendment filed 4/22/02 is objected to under 35 U.S.C. 132 because it introduces new matter into the disclosure. 35 U.S.C. 132 states that no amendment shall introduce new matter into the disclosure of the invention. The added material which is not supported by the original disclosure is as follows: the amendments to 49 which changes nucleotide sequences; a nucleotide sequence on page 56.

Applicant is required to cancel the new matter in the reply to this Office Action.

Double Patenting

A rejection based on double patenting of the "same invention" type finds its support in the language of 35 U.S.C. 101 which states that "whoever invents or discovers any new and useful process ... may obtain a patent therefor ..." (Emphasis added). Thus, the term "same invention," in this context, means an invention drawn to identical subject matter. See *Miller v. Eagle Mfg. Co.*, 151 U.S. 186 (1894); *In re Ockert*, 245 F.2d 467, 114 USPQ 330 (CCPA 1957); and *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970).

A statutory type (35 U.S.C. 101) double patenting rejection can be overcome by canceling or amending the conflicting claims so they are no longer coextensive in scope. The filing of a terminal disclaimer cannot overcome a double patenting rejection based upon 35 U.S.C. 101.

Claims 36 is provisionally rejected under 35 U.S.C. 101 as claiming the same invention as that of claim 36 of copending Application No. 10/364,649. This is a provisional double patenting rejection since the conflicting claim has not in fact been patented.

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claim 37 is provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649. Although the conflicting claims are not identical, they are not patentably distinct from each other because the instant claim 37 recites beta glucuronidase which is encompassed by the beta-glucuronidases recited in copending 10/364,649, claim 36, since an isolated beta glucuronidase having 90% identity with the sequence shown in SEQ ID NO:6, would be encoded by a nucleic acid molecule that would hybridize under stringent conditions to the complement of nucleotides 1-1689 of SEQ ID NO:14.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Claims 60-63 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649 in view of Hochuli et al. (Bio/Technology 6:1321-1325, 1988)

Claim 36 of copending application 10/364,649 teaches an isolated beta-glucuronidase encoded by a nucleic acid molecule comprising nucleotides 1-1689 of Figure 4I-J (SEQ ID NO:14) or by a nucleic acid molecule that hybridizes under stringent conditions to the complement of said nucleic acid molecule. This nucleic acid molecule, and the beta-glucuronidase encoded by it, is the same as that disclosed in

Fig. 4I-J, or SEQ ID NO:14 of the instant application (nucleic acid) and SEQ ID NO:6 (protein).

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be hexa-His.

However, Hochuli et al. disclose protein fusions between a protein of interest, and a peptide of six histidine residues, i.e. "hexa-His", and the usefulness of said fusion protein for purification of the protein of interest (see . It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase of SEQ ID NO:14 in the US patent application 10/364,649, by fusing it to a peptide such as hexa-His, as taught by Hochuli et al., since the references generally concern the production and isolation of proteins of interest using genetic techniques, and since Hochuli et al. teach general techniques that are known in the art to be useful for isolation of proteins of interest or for bioassays. One would have been motivated to do so by the desire to obtain in purified form, the protein of interest which is disclosed by the US patent application, 10/364,649, since it is well known in the art that purified products have the advantage of lack of contaminants. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

This is a provisional obviousness-type double patenting rejection.

Claims 60-63 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649 in view of Diamandis et al. (Clin. Chem. 37, 625, 1991) (cited by applicants).

Claim 36 of copending application 10/364,649 teaches an isolated beta-glucuronidase encoded by a nucleic acid molecule comprising nucleotides 1-1689 of Figure 4I-J (SEQ ID NO:14) or by a nucleic acid molecule that hybridizes under stringent conditions to the complement of said nucleic acid molecule. This nucleic acid molecule, and the beta-glucuronidase encoded by it, is the same as that disclosed in Fig. 4I-J, or SEQ ID NO:14 of the instant application (nucleic acid) and SEQ ID NO:6 (protein).

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be streptavidin.

However, Diamandis et al. teach fusion proteins between an enzyme of interest and streptavidin, and the usefulness of said fusion protein for such applications as immunoassays, flow cytometry, cell sorting, and Western blots (see Table 2 and pages 631-634). It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase of SEQ ID NO:14 in the US patent application 10/364,649, by fusing it to a peptide such as streptavidin, as taught by Diamandis et al., since the references concern enzymes of interest, and since Diamandis et al. teach general techniques of making enzyme- streptavidin fusions that

Art Unit: 1636

are known in the art to be applicable to enzymes whose activity is known, for use in bioassays. One would have been motivated to do so by the desire to obtain a beta-glucuronidase fusion useful for assays such as immunoassays. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

This is a provisional obviousness-type double patenting rejection.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 36, 37, and 60 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. (Nature, 399, 323-3329, 1999) in view of Jefferson et al. (GB 2 197 653, cited by applicants).

Nelson et al. disclose a beta-glucuronidase from *Thermatoga maritima*, which is encoded by a nucleic acid molecule comprising nucleotides 1-1689 of SEQ ID NO:14 of the instant application, or which comprises the amino acid sequence of SEQ ID NO:6 of the instant application (see attached sequence alignments). The difference between the reference and the instant application is that the beta-glucuronidase is isolated.

However, Jefferson et al. disclose the isolation of beta-glucuronidase from a bacteria (see pages 12, 16-17). It would have been obvious to one of ordinary skill in the art, to have isolated the beta-glucuronidase which is disclosed by Nelson et al. using such well known techniques as that disclosed by Jefferson for the isolation of beta-glucuronidase, since both references disclose beta-glucuronidases from bacteria and their sequences. One would have been motivated to do so by the well known usefulness of purified or isolated proteins, which are free of contaminants and thus in a useful form.

Claims 36, 37, 60-63 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. in view of Jefferson et al. as applied to claims 36 and 37 above, and further in view of Hochuli et al. (Bio/Technology 6:1321-1325, 1988).

Nelson et al. and Jefferson et al. are cited for the reasons set forth above.

The difference between the references and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be hexa-His.

However, Hochuli et al. disclose protein fusions between a protein of interest, and a peptide of six histidine residues, i.e. "hexa-His", and the usefulness of said fusion protein for purification of the protein of interest (see . It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase taught by Nelson et al and Jefferson, by fusing it to a peptide such as hexa-His, as taught by Hochuli et al., since the references generally concern the

Art Unit: 1636

production and isolation of proteins of interest using genetic techniques, and since Hochuli et al. teach general techniques that are known in the art to be useful for isolation of proteins of interest or for bioassays. One would have been motivated to do so by the desire to obtain in purified form, the protein of interest which is disclosed by the US patent application, 10/364,649, since it is well known in the art that purified products have the advantage of lack of contaminants. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

Claims 36, 37, 60-63 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. in view of Jefferson et al. as applied to claims 36 and 37 above, and further in view of Diamandis et al. (Clin. Chem. 37, 625, 1991) (cited by applicants).

Nelson et al. and Jefferson et al. are cited for the reasons set forth above.

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be streptavidin.

However, Diamandis et al. teach fusion proteins between an enzyme of interest and streptavidin, and the usefulness of said fusion protein for such applications as immunoassays, flow cytometry, cell sorting, and Western blots (see Table 2 and pages 631-634). It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase as taught by Nelson et al. and

Art Unit: 1636

Jefferson, by fusing it to a peptide such as streptavidin, as taught by Diamandis et al., since the references concern enzymes of interest, and since Diamandis et al. teach general techniques of making enzyme- streptavidin fusions that are known in the art to be applicable to enzymes whose activity is known, for use in bioassays. One would have been motivated to do so by the desire to obtain a beta-glucuronidase fusion useful for assays such as immunoassays. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

Conclusion

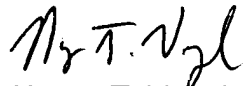
No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nancy T. Vogel whose telephone number is (571) 272-0780. The examiner can normally be reached on 7:00 - 3:30, Monday - Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Irem Yucel, Ph.D. can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Art Unit: 1636

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Nancy T. Vogel, Ph.D.
Patent Examiner

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2005, 05:57:45 ; Search time 100 Seconds
(without alignments)
3239.359 Million cell updates/sec

Title: US-09-936-759-6
Perfect score: 3001
Sequence: 1 MVRPQRNKRFFILINGVWN.....TRDRQPKLVAVLRRLMSEV 563

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 57537466 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	99.9	563	2	Q9X0F2 thermotoga
2	1011	33.7	570	2	Q97U11 sulfolobus
3	977.5	32.6	599	2	Q8XP19 clostridium
4	972.5	32.4	599	2	Q8VNV4 clostridium
5	929	31.0	602	2	Q9AF42 staphylococ
6	919.5	30.6	598	2	Q9AHJ8 lactobacilli
7	906	30.2	670	2	Q6NL66 drosophila
8	906	30.2	670	2	AA693746 drosophila
9	905	30.2	656	2	Q9V8R0 drosophila
10	905	30.2	670	2	Q8MMB7 drosophila
11	902.5	30.1	648	1	Q9V8R0 drosophila
12	899.5	30.0	648	1	Q6LRIO mus musculus
13	898	29.9	651	1	Q6LR FELCA
14	894.5	29.8	648	1	BGIR RAT
15	888	29.6	651	1	BGIR CANFA
16	882	29.4	603	2	Q93VY4 arabidopsis
17	880	29.3	603	2	Q8FHA3
18	879	29.3	603	1	BGIR ECOLI
19	879	29.3	603	2	Q9AHJ4
20	872.5	29.1	648	1	BGIR CERAE
21	865.5	28.8	651	1	BGIR HUMAN
22	865.5	28.8	651	2	AAQ96851
23	862	28.7	628	2	Q95Q32
24	861.5	28.7	603	2	Q6W7J7
25	861.5	28.7	603	2	AAQ76046
26	856.5	28.5	608	2	Q7TPJ3
27	841.5	28.0	686	2	Q9V9T9
28	826.5	27.5	599	2	Q8E6A6
29	821.5	27.4	599	2	Q8E0N2
30	811	27.0	567	2	Q7UCR6
31	809	27.0	567	2	Q63RC5

32	728	24.3	660	2	Q7PEZ2	Q7PEZ2 anophelis g
33	691	23.0	368	2	Q8X671	Q8X671 escherichia
34	691	23.0	370	2	Q7AD15	Q7AD15 escherichia
35	531	17.7	459	2	Q8FMX0	Q8FMX0 cornebacte
36	487	16.2	755	2	Q92XF7	Q92XF7 rhizobium m
37	486.5	16.2	745	2	Q93IM0	Q93IM0 thermoaer
38	482	16.1	716	1	BGAL_THERU	BGAL_THERU
39	482	16.1	716	2	CAA38462	CAA38462 thermoaer
40	481.5	16.0	998	1	BGAL_LACUA	Q48727 lactococcus
41	477.5	15.9	998	2	Q8VPU3	Q8VPU3 lactococcus
42	476.5	15.9	1085	2	Q85250	Q85250 thermotoga
43	472.5	15.7	996	2	Q87523	Q87523 lactococcus
44	460	15.3	743	1	BGAL_THERT	P77989 thermoaer
45	452.5	15.1	1084	1	BGAL_THERMA	Q56307 thermotoga

ALIGNMENTS

ID	Q9X0F2	PRELIMINARY;	PRT;	563 AA.
AC	Q9X0F2			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Beta-glucuronidase.			
GN	OrderedLocNames=TW1062;			
OS	Thermotoga maritima.			
OC	Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.			
OX	NCBI_TaxID=2336;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MSB8 / DSM 3109 / ATCC 43589;			
RX	MEBLIN=99287316; PubMed=10360571; DOI=10.1038/20601.			
RA	Nelson K.E., Clayton R.A., Gill S.R., Gwim M.L., Dodson R.J.,			
RA	Halt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,			
RA	McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,			
RA	Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,			
RA	Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,			
RA	Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,			
RT	"Evidence for lateral gene transfer between Archaea and Bacteria from			
RT	genome sequence of Thermotoga maritima."			
RL	Nature 399:323-329 (1999).			
DR	EMBL; AE001766; AA036143.1; ..			
DR	PIR; A72300; A72300.			
DR	HSSP; P08236; 1BHG.			
DR	TIGR; TM1062; ..			
DR	GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl ..; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR008979; Gal bind like.			
DR	InterPro; IPR006101; Glyco_hydro_2.			
DR	InterPro; IPR006102; Glyco_hydro_2ig.			
DR	InterPro; IPR006104; Glyco_hydro_2SB.			
DR	InterPro; IPR006103; Glyco_hydro_2TIM.			
DR	Pfam; PF00703; Glyco_hydro_2; 1.			
DR	Pfam; PF02836; Glyco_hydro_2_C; 1.			
DR	Pfam; PF02837; Glyco_hydro_2_N; 1.			
DR	PRINTS; PR00132; GHYDRLASE2.			
DR	PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.			
KW	Complete proteome.			
SO	SEQUENCE 563 AA; 65682 MW; 98C030875D33B6C1 CRC64;			
Query Match	99.8%; Score 2999; DB 2; Length 563;			
Best Local Similarity	99.8%; Pred. No. 4,1e-190;			
Matches	562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 MVRPQRNKRFFILINGVWNLEVTSKDRPIAVPGSNWEQYQDCYEGEPFTYKTFVVPK 60			
Db	1 MVRPQRNKRFFILINGVWNLEVTSKDRPIAVPGSNWEQYQDCYEGEPFTYKTFVVPK 60			
Qy	61 XLGSKIRLYFAAVNTDCEVFLNGEKVGNHIEYLPPEVDVTGKVGXGNEELRVVENRL 120			

```

Db      61 ELGQKHRLVFAAVNTDCEVFLNGEKVGENHIEVLPFEVDVTVGKVGSGENELRVVENRL 120
Qy      121 KVGGFPSKVPDGGTHVGVFGSGFPFPPANPDPFPYGGIIRPVLIIEFTDHARILDIWDTSES 180
Db      121 KVGGFPSKVPDGGTHVGVFGSGFPFPPANPDPFPYGGIIRPVLIIEFTDHARILDIWDTSES 180
Qy      181 EPEKKLGKVKVKIIEVSEAVGQEMTILGEEKKIRFNSNFVEGEFTLENARFVSLDEPY 240
Db      181 EPEKKLGKVKVKIIEVSEAVGQEMTILGEEKKIRFNSNFVEGEFTLENARFVSLDEPY 240
Qy      241 LYLKYLEKDEYTLDIGIRTIISWDEKRLYLNGKVPFLKGFKEEPPVLGOGTFYPLMI 300
Db      241 LYLKYLEKDEYTLDIGIRTIISWDEKRLYLNGKVPFLKGFKEEPPVLGOGTFYPLMI 300
Qy      301 KDFNLLKMINANSFRTSHYPSYSEEMDLADRLGILVIDEAPHVIGITRYHYNPETOKIAD 360
Db      301 KDFNLLKMINANSFRTSHYPSYSEEMDLADRLGILVIDEAPHVIGITRYHYNPETOKIAD 360
Qy      361 NIKRMIDRHKNHPSVIMWSVANEESNHPDAEGFKALEYTANEMDTRVVMVSMMDAP 420
Db      361 NIKRMIDRHKNHPSVIMWSVANEESNHPDAEGFKALEYTANEMDTRVVMVSMMDAP 420
Qy      421 DEKTRDVALKYFDIVCVNRYGYWYIYQRIIEBGLQALEKDIIEELYARHKRPIFVTEFGAD 480
Db      421 DEKTRDVALKYFDIVCVNRYGYWYIYQRIIEBGLQALEKDIIEELYARHKRPIFVTEFGAD 480
Qy      481 AINGIHDPQMFSEYQAEVLEKTRILLKQDIYIGTHVAFADFKTPONVRRPILNHK 540
Db      481 AINGIHDPQMFSEYQAEVLEKTRILLKQDIYIGTHVAFADFKTPONVRRPILNHK 540
Qy      541 GVFTDRQPKLVAVHLRLMSEV 563
Db      541 GVFTDRQPKLVAVHLRLMSEV 563

```

RESULT 2

```

097U11 PRELIMINARY; PRT; 570 AA.
AC 097U11
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-glucuronidase (Gusb) (EC 3.2.1.31).
GN Name-gusb, OrderedlocusNames=SS03036;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
NCBI_Taxid=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA Shew Q., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,
RA Aweez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moore A., Brauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.B., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL, AF006894; AAK4138.1; -.
DR PIR, C90485; C90485.
DR HSSP, P08236; 1BHG.
DR GO, GO:0004566; F:beta-glucuronidase activity; IEA.
DR GO, GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro, IPR008979; Gal_bind_like.
DR InterPro, IPR006101; Glyco_hydro_2.
DR InterPro, IPR006102; Glyco_hydro_2.
DR InterPro, IPR006104; Glyco_hydro_2B.
DR InterPro, IPR006103; Glyco_hydro_2T1M.
DR Pfam, PF00703; Glyco_hydro_2; 1.
DR Pfam, PF02836; Glyco_hydro_2_C; 1.

```

```

DR Pfam, PF02837; Glyco_hydro_2_N; 1.
DR PRINTS; PR00132; GLHIDRLASE2.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 570 AA; 66795 MW; DEB3FEC8050AF189 CRC64;

```

```

Query Match      33.7%; Score 1011; DB 2; Length 570;
Best Local Similarity 39.2%; Pred. No. 1.7e-58;
Matches 230; Conservative 92; Mismatches 191; Indels 74; Gaps 14;

```

```

Qy      15 LAGVNLLEVTSKDRP-----IAVGSNNEQYODLCYDEGFTYKTTVYVK 60
Db      11 LQGFMKFKIDNENGTGENGMKGLSESDIITYPASNEONPKMDQSGIAMVOKDLPVSN 70
Qy      61 XLSQKHRLVFAAVNTDCEVFLNGEKVGENHIEVLPFEVDVTVGKVGSGENELRVVENRL 120
Db      71 DNGNRKAMVVEGAGYITKLMTINGEYGTGHEGSPFOGFKPIKLKV---NEFNKIV---V 123
Qy      121 KVGGFPSKVPDGGTHVGVFGSGFPFPPAN-----PDPFPYGGIIRPVLIIEFTDHARILDIW 174
Db      124 KIDNTPSPY-----NLPPARDLNMAFDFFNNGGIHRPYIIEFVDECHVEDIT 171
Qy      175 VDTSESEPEKKLGKVKIIEVSEAVGQEMTILGEEKKI-----RTSNRPFEGEFTLEN 230
Db      172 VYT-----KSYGHLKVEL-LSBCNQRFSRLKLVDEGRVILNESSNVEFEKD--VNN 222
Qy      231 ARFWSLEDYLYPLKYLE-----KDEYTLDIGIRTIISWDEKRLYLNGKVPFLKGFKE 285
Db      223 VLPWSPDNFYLYTLVEMVVGGLKDSVYERIGFQDVEYKDGKTYLNGKPIFLKGFGRHE 282
Qy      286 EFPVLGQGFYPLMIKDFNLLKMINANSFRTSHYPSYSEEMDLADRLGILVIDEAP--HV 343
Db      283 DEPIILGKFTYGAVALVARDFYLMRKIGANSFRTSHYPSNHLADLMGLVILIEPPLCYS 342
Qy      344 GTRHYHNPETOKI-----AEDNIRMIIDRHKNHPSVIMWSVANEESNHPDAEGF 394
Db      343 NISRWVSGEIAKMGQDVYFEKQVDTIKEMIRQHKNRSVIMWSVANEPPSDIEVAEF 402
Qy      395 FPALEYTANEMDTRVVMVSMMDAPDEKTRDVALKYFDIVCVNRYGYWYIYQRIIEBGL 454
Db      403 IRREVELFKSLDSSRPVTPAS-----HRSVRDLALEYVDVILSNYHGYTEMGIDSGV 457
Qy      455 QALEKDIEELVARRH-RKPIFVTEFGADAIAGIHYPPQMFSEYQAEVLEKTRILLKQD 513
Db      456 KVALELEIEIRHKKPEKPIITTEFGADATYGLSDPPQMFSEYQAEVLEKTRILLKQD 517
Qy      514 YIIGTHVAFADFKTPONVRRPILNHKGVFTDRQPKLVAVHLRLM 560
Db      518 YIVGFHINMFADFKTPONRSRTILNRKGIIFTDRQPKLAAKVVEELF 564

```

RESULT 3

```

08XP19 PRELIMINARY; PRT; 599 AA.
AC 08XP19
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-glucuronidase.
GN Name-bglr, OrderedlocusNames=CPE0147;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_Taxid=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL, AF003185; BAB79853.1; -.

```

Wed Jan 26

Db 211 TTCTCCACGAGAGAAATGGGAGAGATGACATTGAATACCTTCCCTTCAGATGAT 300
 Qy 301 GTGACGGGAAAAGTAAATCCGAGAGAACAACTCAGGGTGGTTGGAGAACGATTG 360
 Db 301 GTGACGGGAAAAGTAAATCCGAGAGAACAACTCAGGGTGGTTGGAGAACGATTG 360
 Qy 361 AAAGTGGGAGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTT 420
 Db 361 AAAGTGGGAGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTT 420
 Qy 421 GGAAGTTTCCACCTGCAAACTTCGACTTTCCTCCCTACGGTGAATCATTAAGCCTGTT 480
 Db 421 GGAAGTTTCCACCTGCAAACTTCGACTTTCCTCCCTACGGTGAATCATTAAGCCTGTT 480
 Qy 481 CTGATAGAGTTCCAGACCAACGAGAGATCTCGACATCTGGGTGACACGATGAGTCT 540
 Db 481 CTGATAGAGTTCCAGACCAACGAGAGATCTCGACATCTGGGTGACACGATGAGTCT 540
 Qy 541 GAAACCGAGAGAACTTGGAAAAGTGAAGATAGAACTTCAGAAAGCGGTG 600
 Db 541 GAAACCGAGAGAACTTGGAAAAGTGAAGATAGAACTTCAGAAAGCGGTG 600
 Qy 601 GGACAGAGATGACGATCAAACTTGGAGAGAAAGAAAAGATTAGAACATCCACAGA 660
 Db 601 GGACAGAGATGACGATCAAACTTGGAGAGAAAGAAAAGATTAGAACATCCACAGA 660
 Qy 661 TTGCTGAGAGAGGATTCATCTCTGAAAAGCCGAGGTTCTGGAGCCTCGAAGATCCAT 720
 Db 661 TTGCTGAGAGAGGATTCATCTCTGAAAAGCCGAGGTTCTGGAGCCTCGAAGATCCAT 720
 Qy 721 CTTTATCTCTCAAGGTGGAACCTTGAAGAAAGACGATGACATCTGCAATCGAATGAGA 780
 Db 721 CTTTATCTCTCAAGGTGGAACCTTGAAGAAAGACGATGACATCTGCAATCGAATGAGA 780
 Qy 781 ACGATGAGTGGAGAGAGAGAGGCTCTATCTGAACGGGAAACCTGCTTTTGAAGGCG 840
 Db 781 ACGATGAGTGGAGAGAGAGAGGCTCTATCTGAACGGGAAACCTGCTTTTGAAGGCG 840
 Qy 841 TTGGAAGACAGAGAAATCCCGTTCCTGGGAGCGGCACTTTATCCATTTGATGATA 900
 Db 841 TTGGAAGACAGAGAAATCCCGTTCCTGGGAGCGGCACTTTATCCATTTGATGATA 900
 Qy 901 AAAGCTTCAACCTTGAAGTGAATCAACGGAATCTTTCAGAGACCTTCATATCTCT 960
 Db 901 AAAGCTTCAACCTTGAAGTGAATCAACGGAATCTTTCAGAGACCTTCATATCTCT 960
 Qy 961 TACAGTGAAGAGTGGCTGATCTTTCGAGACAGACTCGGAATCTTGTGATGAGAGAGCC 1020
 Db 961 TACAGTGAAGAGTGGCTGATCTTTCGAGACAGACTCGGAATCTTGTGATGAGAGAGCC 1020
 Qy 1021 CCGCAGCTTGTATCAACAGGTAACCACTCAATCCCGAGACTCAGAGATGACAGAGAGC 1080
 Db 1021 CCGCAGCTTGTATCAACAGGTAACCACTCAATCCCGAGACTCAGAGATGACAGAGAGC 1080
 Qy 1081 AACATPAGAGAGATGATGACAGACAGACAGAACATCCAGTGTATCATGTGAGAGTGTG 1140
 Db 1081 AACATPAGAGAGATGATGACAGACAGACAGAACATCCAGTGTATCATGTGAGAGTGTG 1140
 Qy 1141 GCGAAGCAAGAGTCCAAACATCCAGACGCGAGAGGTTTCTTCAAGCCCTTTATGAG 1200
 Db 1141 GCGAAGCAAGAGTCCAAACATCCAGACGCGAGAGGTTTCTTCAAGCCCTTTATGAG 1200
 Qy 1201 ACTGCCAATGAATGATGACACACGCCCCGTTGTATGATGATGATGACGACAGCA 1260
 Db 1201 ACTGCCAATGAATGATGACACACGCCCCGTTGTATGATGATGATGACGACAGCA 1260
 Qy 1261 GACGAGAGACAGAGAGCTGCGCTGAGATGATCTTCAGATCTGTGTGTGAACAGGTAC 1320
 Db 1261 GACGAGAGACAGAGAGCTGCGCTGAGATGATCTTCAGATCTGTGTGTGAACAGGTAC 1320
 Qy 1321 TACGCTGTATCATCTATCAGGAGAGATGAGAGAGACTTCAAGCTTCGAAAAGAC 1380
 Db 1321 TACGCTGTATCATCTATCAGGAGAGATGAGAGAGACTTCAAGCTTCGAAAAGAC 1380

Db 1321 TACGCTGTATCATCTATCAGGAGAGATGAGAGAGACTTCAAGCTTCGAAAAGAC 1380
 Qy 1381 ATAGAAAGCTCTATGCAAGGACAGAAAGCCATCTTTGTGACAGAAATTCGTGCGGAC 1440
 Db 1381 ATAGAAAGCTCTATGCAAGGACAGAAAGCCATCTTTGTGACAGAAATTCGTGCGGAC 1440
 Qy 1441 GCGATAGCTGACATCCATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1441 GCGATAGCTGACATCCATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Qy 1501 CTGCTTGAAGAGACGATCAGGCTCTTTTGAAGAAAAGATCATGATGAGAACACAGCTG 1560
 Db 1501 CTGCTTGAAGAGACGATCAGGCTCTTTTGAAGAAAAGATCATGATGAGAACACAGCTG 1560
 Qy 1561 TGGGCTTTCAGATTTTAAAGCTCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 Db 1561 TGGGCTTTCAGATTTTAAAGCTCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 Qy 1621 GGTGTTTTCAGAGAGACAGAACCAACCTGTTGCTCATGATGATGAGAGAGAGAGAGAG 1680
 Db 1621 GGTGTTTTCAGAGAGACAGAACCAACCTGTTGCTCATGATGATGAGAGAGAGAGAGAG 1680
 Qy 1681 AGTGAAGTT 1689
 Db 1681 AGTGAAGTT 1689

RESULT 2
 AE001766/c 12583 bp DNA linear BCT 04-JUN-2004
 LOCUS Thermotoga maritima MSB8 section 78 of 136 of the complete genome.
 DEFINITION
 ACCESSION AE001766 AE000512
 VERSION AE001766.1 GI:4981600
 KEYWORDS
 SOURCE Thermotoga maritima MSB8
 ORGANISM Thermotoga maritima MSB8
 Bacteria; Thermotogales; Thermotogaceae; Thermotoga.

REFERENCE
 AUTHORS Nelson, K.E., Clayton, R.A., Gill, S.R., Gwyn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., Eisen, J.A., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
 Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima
 Nature 399 (6734), 323-329 (1999)

TITLE
 JOURNAL
 FEATURES
 source 2 (bases 1 to 12583)
 JOURNAL MEDLINE 99287316
 PUBMED 10360571
 REFERENCE
 AUTHORS Nelson, K.E., Clayton, R.A., Gill, S.R., Gwyn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
 Direct Submission
 Submitted (01-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 Location/Qualifiers
 1..12583
 /organism="Thermotoga maritima MSB8"
 /mol_type="genomic DNA"
 /strain="MSB8"
 /db_xref="taxon:243274"
 81..1607
 /locus_tag="TM1058"
 81..1607
 /locus_tag="TM1058"
 /note="similar to GB:AE000566 percent identity: 48.70; identified by sequence similarity; putative"
 /codon_start=1

TITLE
 JOURNAL
 FEATURES
 source 2 (bases 1 to 12583)
 JOURNAL MEDLINE 99287316
 PUBMED 10360571
 REFERENCE
 AUTHORS Nelson, K.E., Clayton, R.A., Gill, S.R., Gwyn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
 Direct Submission
 Submitted (01-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 Location/Qualifiers
 1..12583
 /organism="Thermotoga maritima MSB8"
 /mol_type="genomic DNA"
 /strain="MSB8"
 /db_xref="taxon:243274"
 81..1607
 /locus_tag="TM1058"
 81..1607
 /locus_tag="TM1058"
 /note="similar to GB:AE000566 percent identity: 48.70; identified by sequence similarity; putative"
 /codon_start=1

gene
CDS
complement (1650..1913)
/locus_tag="TM1059"
/complement (1650..1913)
/locus_tag="TM1059"
/note="similar to SP:P45693 PID:862985 GB:AL009126 percent identity: 48.70; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="spovs-related protein"
/protein_id="AAD36136.1"
/db_xref="GI:4981602"
/translation="MEVLKVSQSDPNKAVAGAVREHKAELQALGAGVNOAVK AIAAGVLAGSDLVPAFPAFVDEIEKRAIKFIVPKS"
/locus_tag="TM1060"
/complement (1962..3272)
/locus_tag="TM1060"
/complement (1962..3272)
/locus_tag="TM1060"
/note="similar to GB:AE000782 percent identity: 49.74; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="conserved hypothetical protein"
/protein_id="AAD36144.1"
/db_xref="GI:4981610"
/translation="MNISIIIEGALAVLINQFPGGAVLTGYFLMNGASSFTIGLFGSIP FLANTQLTSPFHSRKRKQIIVPLMTATSIILFAVPAIKHGLLALYLLFYI QIAGASAPLMQSGMSDLPKMDISYEGFENLHGAVQIPAMFLAGAIIDSIGENK GFGTLFAGSLGANGYFLKIQEYEPYKREASVITKAVKFLKEHEKFLFPGA FNNFAIGVTVYINMLLKEVESYLOISVNAVGMFICTLFOPFMGLDPRGVFOYF LKVCILHAIYILMTLTPRSFLYFLQIIIGLIVTAGISQVLYTFLMTAPSSLYT EAFVSFSLNLSFAGSLVASVLALENISLPPGSAIRLITWISFPLASAAVYII SRMLGTPQKVDLSIQAKESFSGGTVPWIRERLNTINIFRRK"

gene
CDS
complement (3382..4545)
/locus_tag="TM1061"
/complement (3382..4545)
/locus_tag="TM1061"
/note="similar to percent identity: 0.00; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAD36137.1"
/db_xref="GI:4981603"
/translation="WRSMTPVRRWYISILRKICEMPLECASDRLKKSMPVEGKSEK RRPFLHELGRIFCGISPFELNESPSTDEBKRIATRLSEPAVKSIVAVTNCK RYMPKEGRQPLVDAAFLVEALIRAPKYLMEGLDSTKRLIRLAKTRKLEPSNM LLFSAMIEFFPFGAGEMDSTVDLILKNVESWYVAGGCGPFRMDVNSPFIYV MIDVARISEKTEWELKLVYVLRRAQYAVLRKMSPEGTFFPIGSIITRYAVF HILSOLSLHLIPASPAQVCAITAVARIIFENSTPDENGWMLKIGVISQPSLGE EYITTSGLYCTVPLPIGLPTSPDFMRPCKMTKVKVGEDEVAPDRALND"

gene
CDS
complement (4542..6233)
/locus_tag="TM1062"
/complement (4542..6233)
/locus_tag="TM1062"
/note="similar to PID:642973 PID:14446 PID:413358 percent identity: 57.73; identified by sequence similarity; putative"
/codon_start=1

gene
CDS
complement (6284..7309)
/locus_tag="TM1063"
/complement (6284..7309)
/locus_tag="TM1063"
/note="similar to SP:P42065 PID:677944 GB:AL009126 percent identity: 75.31; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="oligopeptide ABC transporter, ATP-binding protein"
/protein_id="AAD36138.1"
/db_xref="GI:4981604"
/translation="WALDEVKNLKKYFPPIIKGRFRKVVYIKAVDQISFHEBGETL GLVSGGCTTAKLIMRGIEPTEGEIVLNDGKRVITKSEKELBKVRRLQIM IFODPYSINPMWTARDIJAEPVNVYIKGKEIDAVSDLRVAGRPVWQYPH AFSGGQRORIALAIALKALKVLCDPEPLADVVOQIINLLADLOKENVLYLFI SHDLGVEHITNRVAVMYGRVLEALREBELFSSRKPTEALLSAVPDPKRRKK AOLTEGVPDPSNPBGCFHPRCPYAKALCKEYVYEDLNRVGDQNPHLVACHFADSLK LEGVGTM"
complement (7296..8294)
/locus_tag="TM1064"
/complement (7296..8294)
/locus_tag="TM1064"
/note="similar to SP:P42064 PID:677943 GB:AL009126 percent identity: 72.95; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="oligopeptide ABC transporter, ATP-binding protein"
/protein_id="AAD36139.1"
/db_xref="GI:4981605"
/translation="WSTLQIKNLRTYFPTDEGVAVAVDSFSEIEGRITLVGVBEG CGKSVTRRSIKLSTAGRIVSGEILYNMGOMVDVFSKEIRKVRGHIAMIQES PMAFSPVYITIGDITBGMLYHNGITQGEAREBAVELLRVGIPEKMDISYFEYS GGRORAMIMALSCNRLIADPPTALVTOAOVTLDKLOOEYKMAIMITN MGVAEMADHVVMYVGRVESAPEVELFYNPHVYSLLSRSIPYVGRVERLEVE GDVDDPNMRKCGFHRPCYMMKGIQDEREPEVEVEPEHRVSCFLYGBKDGAS"

gene
CDS
complement (8306..9409)
/locus_tag="TM1065"
/complement (8306..9409)
/locus_tag="TM1065"
/note="similar to GB:AE006657 percent identity: 67.80; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="oligopeptide ABC transporter, permease protein"
/protein_id="AAD36140.1"
/db_xref="GI:4981606"
/translation="MKKEOMEKEEFYVASQWQIMWRFRKHLAVIGCVLLIYVFA IFCREFAVDNKNKYRVPVAPORIFHEHSGKFGPVPVYATVVDLETIRIYKED KSKLIRKIFPRGDEYKRWGIMKGNINIHIGVEDGMFLGDSIGRMDLSRIYGARL STSILIGVFLSFLIGVAIGSIGREGAVUNFQRTTEIISITIPIMLALSAALP QNMPPLRVYFVIVILSTGWTDLAVVRSRPLSREBDPMAAKFMGASERARIFRH MLPSVMSHLIASITLSIGMILGETSLSFLGGLKPVISGVCLIQEONLTVALYV WLLIPVAVITVLCFNFVGDGLRDAADPYANM"

gene
CDS
complement (9420..10403)
/locus_tag="TM1066"
/complement (9420..10403)
/locus_tag="TM1066"

CDS
 complement(9420..10403)
 /locus tag="TM1066"
 /notes similar to SP:P42062 PID:677946 GB:AL009126 percent
 identity: 62.93; identified by sequence similarity;
 putative"
 /codon_start=1
 /transl_table=11
 /product="oligopeptide ABC transporter, permease protein"
 /protein_id="ABD36141.1"
 /db_xref="GI:4981607"

Query Match 99.9%; Score 1688; DB 1; Length 12583;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1688; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTAAGACCCGACAGAAACAAGAGATTATTTCTTATCTTGATGAGTTGGAAAT 60
 DB 6233 ATGCTAAGACCCGACAGAAACAAGAGATTATTTCTTATCTTGATGAGTTGGAAAT 6174
 QY 61 CTGGAAGTAACAGACAGAAAGACCAATCGCGCTTCTGSAAGCTGSAATGACATAC 120
 DB 6173 CTGGAAGTAACAGACAGAAAGACCAATCGCGCTTCTGSAAGCTGSAATGACATAC 6114
 QY 121 CAGGATCTGTGCTACGAGAGAGACCCCTTACCTACAAAACCACTTCTACGTTCCGAAG 180
 DB 6113 CAGGATCTGTGCTACGAGAGAGACCCCTTACCTACAAAACCACTTCTACGTTCCGAAG 6054
 QY 181 NAACTTTCAAAAACAATCACTCACTTTACTTGTCTGCGGTGAACAAGCTTCCAGATC 240
 DB 6053 NAACTTTCAAAAACAATCACTCACTTTACTTGTCTGCGGTGAACAAGCTTCCAGATC 5994
 QY 241 TTCCTCAACGAGAGAAAGTGGAGAGATCACTTGAATACCTTCCCTCGAAGTAAAT 300
 DB 5993 TTCCTCAACGAGAGAAAGTGGAGAGATCACTTGAATACCTTCCCTCGAAGTAAAT 5934
 QY 301 GTGACGGGAGAAAGTGAATCCGAGAGAGACGAATCAGGGGTGTTGTTGAGAACAAGATTG 360
 DB 5933 GTGACGGGAGAAAGTGAATCCGAGAGAGACGAATCAGGGGTGTTGTTGAGAACAAGATTG 5874
 QY 361 AAGAGTGGAGAGATTTCCCTCGAAAGTTCCAGACAGCGGCACTCAACCGTGGGATTTTTT 420
 DB 5873 AAGAGTGGAGAGATTTCCCTCGAAAGTTCCAGACAGCGGCACTCAACCGTGGGATTTTTT 5814
 QY 421 GGAAGTTTCCACCTGCAAACTTCGACTTCTCCCTACGGTGAATCATTAAGGCTGTT 480
 DB 5813 GGAAGTTTCCACCTGCAAACTTTCGACTTCTCCCTACGGTGAATCATTAAGGCTGTT 5754
 QY 481 CTGATAGATTCAAGACCAAGCGAGATATCTGACATCTGGGTGGAACGAGTGAATCT 540
 DB 5753 CTGATAGATTCAAGACCAAGCGAGATATCTGACATCTGGGTGGAACGAGTGAATCT 5694
 QY 541 GAACCGGAGAGAAACCTTGAAAAAGTGAAGATGAAGTCTCAAGAGAACCGGTG 600
 DB 5693 GAACCGGAGAGAAACCTTGAAAAAGTGAAGATGAAGTCTCAAGAGAACCGGTG 5634
 QY 601 GGACAGGAGATGACATCAAACTTGAGAGAGAGAAAAAAGATTGAACATCCCAACGA 660
 DB 5633 GGACAGGAGATGACATCAAACTTGAGAGAGAGAAAAAAGATTGAACATCCCAACGA 5574
 QY 661 TTTCGTGAAGGGAGTTCACTCTCGAAAAAGCCAGGTTCTGAGGCTCGAAGATCCATAT 720
 DB 5573 TTTCGTGAAGGGAGTTCACTCTCGAAAAAGCCAGGTTCTGAGGCTCGAAGATCCATAT 5514
 QY 721 CTTTATCTCTCTCAAGGTGGAATTGAAAAAGAGAGTACACTCTTGAGATCGGAATCAGA 780
 DB 5513 CTTTATCTCTCTCAAGGTGGAATTGAAAAAGAGAGTACACTCTTGAGATCGGAATCAGA 5454
 QY 781 ACGATCAGCTGGAGAGAGAGGCTATCTGAACGGGAACCTGCTTTTGAAGGCG 840
 DB 5453 ACGATCAGCTGGAGAGAGAGGCTATCTGAACGGGAACCTGCTTTTGAAGGCG 5394
 QY 841 TTTGGAAGCAGAGGAATTTCCCGTTCTGGGCGAGGCACTTTTATCATGTGATATA 900

DB 5393 TTTGGAAGCAGAGGAATTCGCCGTTCTGGGGCAGGGCACTTTATCATGTGATATA 5334
 QY 901 AAGACTTCAACCTTCTGATGATGATCAACGGGAATTTCTTACAGACCTCTCATATCTT 960
 DB 5333 AAGACTTCAACCTTCTGATGATGATCAACGGGAATTTCTTACAGACCTCTCATATCTT 5274
 QY 961 TACAGTGAAGAGTGGCTGATCTTTCGACAGACCTCGGAATCTCTTGATGAGAGAGCC 1020
 DB 5273 TACAGTGAAGAGTGGCTGATCTTTCGACAGACCTCGGAATCTCTTGATGAGAGAGCC 5214
 QY 1021 CCGCACTTTGATCAAGGATCACTACATCCCGAGACTCAGAAAGTACAGAAAGC 1080
 DB 5213 CCGCACTTTGATCAAGGATCACTACATCCCGAGACTCAGAAAGTACAGAAAGC 5154
 QY 1081 AACATTAAGAAATGATGACAGACAGAAACCAATCCAGTGTGATCATGTGAGTGTG 1140
 DB 5153 AACATTAAGAAATGATGACAGACAGAAACCAATCCAGTGTGATCATGTGAGTGTG 5094
 QY 1141 GCGAAGCAACAGAGTCCAGACATCGACAGCGGGAGGTTCTTCAAGCCCTTATAG 1200
 DB 5093 GCGAAGCAACAGAGTCCAGACATCGACAGCGGGAGGTTCTTCAAGCCCTTATAG 5034
 QY 1201 ACTGCCAATGAATGATGACAGACAGCGCCGCTTGTATGATGAGCATGATGAGACGACA 1260
 DB 5033 ACTGCCAATGAATGATGACAGACAGCGCCGCTTGTATGATGAGCATGATGAGACGACA 4974
 QY 1261 GACGAGAGACAGAGAGCTGGCGCTGAATCTTCAATCTGTCTGTGTAACAGGTAC 1320
 DB 4973 GACGAGAGACAGAGAGCTGGCGCTGAATCTTCAATCTGTCTGTGTAACAGGTAC 4914
 QY 1321 TACGCTGTGTAATCTATCAAGAGAGATGAAGAGAGCTTCAAGCTCTGAAAAAAGC 1380
 DB 4913 TACGCTGTGTAATCTATCAAGAGAGATGAAGAGAGCTTCAAGCTCTGAAAAAAGC 4854
 QY 1381 ATAGAAGAGCTCTATGCAAGGACAGAAAGCCCATCTTGTGCAAGATTCGTCGCGAC 1440
 DB 4853 ATAGAAGAGCTCTATGCAAGGACAGAAAGCCCATCTTGTGCAAGATTCGTCGCGAC 4794
 QY 1441 GCGATAGCTGGCATCTCACTACATCTCAATATGTTCTCCGAAGATCCAAAGCAGAG 1500
 DB 4793 GCGATAGCTGGCATCTCACTACATCTCAATATGTTCTCCGAAGATCCAAAGCAGAG 4734
 QY 1501 CTCGTTGAAAGAGATGAGGCTCTTTGAAAAAGCTTCAATCATCTGGAACACAGCTG 1560
 DB 4733 CTCGTTGAAAGAGATGAGGCTCTTTGAAAAAGCTTCAATCATCTGGAACACAGCTG 4674
 QY 1561 TGGGCTTTGAGATTTTAAGACTCTCGAATGTCGAAGAACCCATTTCTCAACCAAG 1620
 DB 4673 TGGGCTTTGAGATTTTAAGACTCTCGAATGTCGAAGAACCCATTTCTCAACCAAG 4614
 QY 1621 GGTGTTTCAAGAGACAGACCAACCAACTCGTGTCTATGTACTGAGAAAGCTGTG 1680
 DB 4613 GGTGTTTCAAGAGACAGACCAACCAACTCGTGTCTATGTACTGAGAAAGCTGTG 4554
 QY 1681 AGTAGAGTT 1689
 DB 4553 AGTAGAGTT 4545

RESULT 3
 AF012423
 LOCUS AF012423 2153 bp mRNA linear MAM 09-SEP-1999
 DEFINITION Felis catus beta-glucuronidase (GUSB) mRNA, complete cds.
 ACCESSION AF012423
 VERSION AF012423.1 GI:4102550
 KEYWORDS
 SOURCE
 ORGANISM
 Felis catus (cat)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 REFERENCE
 1 (bases 1 to 2153)
 Fyfe J.C., Kurzhals R.L., Lassaline M.E., Henhorn P.S., Alur P.R.,
 Wang P., Wolfe J.H., Giger U., Haskins M.E., Patterson D.F.,